



#7

# SEQUENCE LISTING

<110> Cases, Sylvaine  
Stone, Scot  
Zhou, Ping  
Farese, Robert V.  
Chi-Liang Eric Yen

<120> DIACYLGLYCEROL O-ACYLTRANSFERASE 2a  
(DGAT2a)

<130> UCAL240CIP

<140> US 10/046,924

<141> 2002-01-14

<150> 60/271,307

<151> 2001-02-23

<150> 09/794,715

<151> 2001-02-26

<160> 18

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<210> 1

<211> 1231

<212> DNA

<213> Homo sapiens

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caccatgtac	atggaggccc	tgggtgaagct	cttcgacaag	cacaagacca	agttcggcct	1140
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<211> 388  
 <212> PRT  
 <213> Homo sapiens

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Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	Ile	Leu	Ser
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Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	Arg	Ser	Lys	Val
	50					55					60				
Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	Trp	Val	Leu	Ser	Phe
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Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	Leu	Met	Tyr	Ile	Phe	Cys
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Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	Tyr	Phe	Thr	Trp	Leu	Val	Phe
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Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	Leu
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Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly	Ala	Asp
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Leu	Val	Pro	Ile	Tyr	Ser	Phe	Gly	Glu	Asn	Glu	Val	Tyr	Lys	Gln	Val
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Ile	Phe	Glu	Glu	Gly	Ser	Trp	Gly	Arg	Trp	Val	Gln	Lys	Lys	Phe	Gln
	290					295					300				
Lys	Tyr	Ile	Gly	Phe	Ala	Pro	Cys	Ile	Phe	His	Gly	Arg	Gly	Leu	Phe
305					310					315					320
Ser	Ser	Asp	Thr	Trp	Gly	Leu	Val	Pro	Tyr	Ser	Lys	Pro	Ile	Thr	Thr
			325						330					335	
Val	Val	Gly	Glu	Pro	Ile	Thr	Ile	Pro	Lys	Leu	Glu	His	Pro	Thr	Gln
			340					345					350		
Gln	Asp	Ile	Asp	Leu	Tyr	His	Thr	Met	Tyr	Met	Glu	Ala	Leu	Val	Lys
		355					360					365			
Leu	Phe	Asp	Lys	His	Lys	Thr	Lys	Phe	Gly	Leu	Pro	Glu	Thr	Glu	Val
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Leu	Glu	Val	Asn												
385															

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<211> 1167  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> misc\_feature  
 <222> (1)...(1167)  
 <223> n = A,T,C or G

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 ggcatgggct ccagcatcct ctcagccctc caagacatct tctctgtcac ctggctcaac 180  
 agatcyaagg tggaaaaaca gctgcaggtc atctcagtac tacaatgggt cctatccttc 240  
 ctgggtgctag gagtggcctg cagtgtcatc ctcatgtaca ccttctgcac agactgctgg 300  
 ctgatatgctg tgctctactt cacctgggctg gcatttgact ggaacacgcc caagaaaggt 360  
 ggcaggagat cgcagtgggt gcgaaactgg gccgtgtggc gctacttccg agactacttt 420  
 cccatccagc tgggtgaagac acacaacctg ctgaccacca ggaactatat ctttggatac 480  
 caccctcatg gcatcatggg cctgggtgcc ttctgtaact tcagcacaga ggctactgaa 540  
 gtcagcaaga agtttccctg cataaggccc tatttggtta cgttggcygg taacttccgg 600  
 atgcctgtgc ttccgcagta cctgatgtct ggaggcatct gccctgtcaa ccgagacacc 660  
 atagactact tgctctccaa gaatgggagt ggcaatgcta tcatcatcgt ggtgggaggt 720  
 gcagctgagt ccctgagctc catgcctggc aagaacgcag tcaccctgaa gaaccgaaa 780  
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 cccatcactg tccccaaagt ggagcaccgc acccagaaag acatcgacct gtaccatgcc 1080  
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 Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser Ile Leu Ser  
 35 40 45  
 Ala Leu Gln Asp Ile Phe Ser Val Thr Trp Leu Asn Arg Ser Lys Val  
 50 55 60  
 Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln Trp Val Leu Ser Phe  
 65 70 75 80  
 Leu Val Leu Gly Val Ala Cys Ser Val Ile Leu Met Tyr Thr Phe Cys  
 85 90 95  
 Thr Asp Cys Trp Leu Ile Ala Val Leu Tyr Phe Thr Trp Leu Ala Phe  
 100 105 110  
 Asp Trp Asn Thr Pro Lys Lys Gly Gly Arg Arg Ser Gln Trp Val Arg  
 115 120 125  
 Asn Trp Ala Val Trp Arg Tyr Phe Arg Asp Tyr Phe Pro Ile Gln Leu  
 130 135 140  
 Val Lys Thr His Asn Leu Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr  
 145 150 155 160

His Pro His Gly Ile Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr  
 165 170 175  
 Glu Ala Thr Glu Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu  
 180 185 190  
 Ala Thr Leu Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu  
 195 200 205  
 Met Ser Gly Gly Ile Cys Leu Val Asn Arg Asp Thr Ile Asp Tyr Leu  
 210 215 220  
 Leu Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly  
 225 230 235 240  
 Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr Leu  
 245 250 255  
 Lys Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly Ala Asp  
 260 265 270  
 Leu Val Pro Thr Tyr Ser Phe Gly Glu Asn Glu Val Tyr Lys Gln Val  
 275 280 285  
 Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Lys Lys Phe Gln Lys  
 290 295 300  
 Tyr Ile Gly Phe Ala Pro Cys Ile Phe His Gly Arg Gly Leu Phe Ser  
 305 310 315 320  
 Ser Asp Thr Trp Gly Leu Val Pro Tyr Ser Lys Pro Ile Thr Thr Val  
 325 330 335  
 Val Gly Glu Pro Ile Thr Val Pro Lys Leu Glu His Pro Thr Gln Lys  
 340 345 350  
 Asp Ile Asp Leu Tyr His Ala Met Tyr Met Glu Ala Leu Val Lys Leu  
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 370 375 380  
 Glu Val Asn  
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 <211> 1008  
 <212> DNA  
 <213> Mus musculus

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 gactggagaa cccagagca aggaggcaga agatggaact gggccaaag ctggcctgtg 240  
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 ccggtttcag tgtctaagga gagtttgtct catgtgctga gcaaggatgg aggtggcaat 540  
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 atctacactg ttgttgccg ccctatccct gttcagcaga ttctgaaccc gacctcagag 900  
 cagattgaag agctgcatca gacataccta gaggagctaa agaaactatt caatgaacac 960  
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<210> 6  
 <211> 335

<212> PRT  
 <213> Mus musculus

<400> 6

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		20					25						30		
Gln	Val	Cys	Ile	Gly	Ile	Met	Val	Met	Leu	Val	Leu	Tyr	Asn	Tyr	Trp
	35					40						45			
Phe	Leu	Tyr	Ile	Pro	Tyr	Leu	Val	Trp	Phe	Tyr	Tyr	Asp	Trp	Arg	Thr
50					55						60				
Pro	Glu	Gln	Gly	Gly	Arg	Arg	Trp	Asn	Trp	Val	Gln	Ser	Trp	Pro	Val
65					70				75						80
Trp	Lys	Tyr	Phe	Lys	Glu	Tyr	Phe	Pro	Ile	Cys	Leu	Val	Lys	Thr	Gln
				85					90					95	
Asp	Leu	Asp	Pro	Gly	His	Asn	Tyr	Ile	Phe	Gly	Phe	His	Pro	His	Gly
			100					105					110		
Ile	Phe	Val	Pro	Gly	Ala	Phe	Gly	Asn	Phe	Cys	Thr	Lys	Tyr	Ser	Asp
	115						120					125			
Phe	Lys	Lys	Leu	Phe	Pro	Gly	Phe	Thr	Ser	Tyr	Leu	His	Val	Ala	Lys
130						135					140				
Ile	Trp	Phe	Cys	Phe	Pro	Leu	Phe	Arg	Glu	Tyr	Leu	Met	Ser	Asn	Gly
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Pro	Val	Ser	Val	Ser	Lys	Glu	Ser	Leu	Ser	His	Val	Leu	Ser	Lys	Asp
				165				170						175	
Gly	Gly	Gly	Asn	Val	Ser	Ile	Ile	Val	Leu	Gly	Gly	Ala	Lys	Glu	Ala
			180					185					190		
Leu	Glu	Ala	His	Pro	Gly	Thr	Phe	Thr	Leu	Cys	Ile	Arg	Gln	Arg	Lys
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Gly	Phe	Val	Lys	Met	Ala	Leu	Thr	His	Gly	Ala	Ser	Leu	Val	Pro	Val
210						215					220				
Phe	Ser	Phe	Gly	Glu	Asn	Asp	Leu	Tyr	Lys	Gln	Ile	Asn	Asn	Pro	Lys
225					230				235						240
Gly	Ser	Trp	Leu	Arg	Thr	Ile	Gln	Asp	Ala	Met	Tyr	Asp	Ser	Met	Gly
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Val	Ala	Leu	Pro	Leu	Ile	Tyr	Ala	Arg	Gly	Ile	Phe	Gln	His	Tyr	Phe
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Gly	Ile	Met	Pro	Tyr	Arg	Lys	Leu	Ile	Tyr	Thr	Val	Val	Gly	Arg	Pro
	275					280						285			
Ile	Pro	Val	Gln	Gln	Ile	Leu	Asn	Pro	Thr	Ser	Glu	Gln	Ile	Glu	Glu
	290					295					300				
Leu	His	Gln	Thr	Tyr	Leu	Glu	Glu	Leu	Lys	Lys	Leu	Phe	Asn	Glu	His
305					310					315					320
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<210> 7  
 <211> 1129  
 <212> DNA  
 <213> Homo sapiens

<400> 7

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aactatttgt	tcctttacat	cccttatttg	atgtggcttt	actttgactg	gcatacccca	240

gagcggaggag	gcaggagatc	cagctggatc	aaaaattgga	ctcttttgaa	acactttaag	300
gactattttc	caattcatct	tatcaaaact	caagatttgg	atccaagtca	caactatata	360
tttgggtttc	accccatgg	aataatggca	gttggagcct	ttgggaattt	ttctgtaaat	420
tattctgact	tcaaggacct	gtttcctggc	tttacttcat	atcttcacgt	gctgccactt	480
tggttctggt	gtcctgtctt	togagaatat	gtgatgagtg	ttgggctggt	ttcagtttcc	540
aagaaaagtg	tgtcctacat	ggtaagcaag	gagggaggtg	gaaacatctc	tgtcattgtc	600
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attccagagc	acgagactct	tgttttaaaa	tgacttgact	ataaaaaaaaa	attaaaaaat	1080
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<210> 8

<211> 334

<212> PRT

<213> Homo sapiens

<400> 8

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		20					25					30			
Met	Ser	Ile	Gly	Ile	Thr	Val	Met	Leu	Ile	Ile	His	Asn	Tyr	Leu	Phe
	35						40					45			
Leu	Tyr	Ile	Pro	Tyr	Leu	Met	Trp	Leu	Tyr	Phe	Asp	Trp	His	Thr	Pro
	50				55						60				
Glu	Arg	Gly	Gly	Arg	Arg	Ser	Ser	Trp	Ile	Lys	Asn	Trp	Thr	Leu	Trp
65				70					75					80	
Lys	His	Phe	Lys	Asp	Tyr	Phe	Pro	Ile	His	Leu	Ile	Lys	Thr	Gln	Asp
			85						90					95	
Leu	Asp	Pro	Ser	His	Asn	Tyr	Ile	Phe	Gly	Phe	His	Pro	His	Gly	Ile
	100							105				110			
Met	Ala	Val	Gly	Ala	Phe	Gly	Asn	Phe	Ser	Val	Asn	Tyr	Ser	Asp	Phe
	115						120					125			
Lys	Asp	Leu	Phe	Pro	Gly	Phe	Thr	Ser	Tyr	Leu	His	Val	Leu	Pro	Leu
	130				135						140				
Trp	Phe	Trp	Cys	Pro	Val	Phe	Arg	Glu	Tyr	Val	Met	Ser	Val	Gly	Leu
145				150					155					160	
Val	Ser	Val	Ser	Lys	Lys	Ser	Val	Ser	Tyr	Met	Val	Ser	Lys	Glu	Gly
			165					170						175	
Gly	Gly	Asn	Ile	Ser	Val	Ile	Val	Leu	Gly	Gly	Ala	Lys	Glu	Ser	Leu
		180						185					190		
Asp	Ala	His	Pro	Gly	Lys	Phe	Thr	Leu	Phe	Ile	Arg	Gln	Arg	Lys	Gly
	195						200					205			
Phe	Val	Lys	Ile	Ala	Leu	Thr	His	Gly	Ala	Ser	Leu	Val	Pro	Val	Val
	210					215					220				
Ser	Phe	Gly	Glu	Asn	Glu	Leu	Phe	Lys	Gln	Thr	Asp	Asn	Pro	Glu	Gly
225				230					235					240	
Ser	Trp	Ile	Arg	Thr	Val	Gln	Asn	Lys	Leu	Gln	Lys	Ile	Met	Gly	Phe
			245					250						255	
Ala	Leu	Pro	Leu	Phe	His	Ala	Arg	Gly	Val	Phe	Gln	Tyr	Asn	Phe	Gly
	260						265					270			
Leu	Met	Thr	Tyr	Arg	Lys	Ala	Ile	His	Thr	Val	Val	Gly	Arg	Pro	Ile

	275					280					285								
Pro	Val	Arg	Gln	Thr	Leu	Asn	Pro	Thr	Gln	Glu	Gln	Ile	Glu	Glu	Leu				
	290					295					300								
His	Gln	Thr	Tyr	Met	Glu	Glu	Leu	Arg	Lys	Leu	Phe	Glu	Glu	His	Lys				
305					310					315					320				
Gly	Lys	Tyr	Gly	Ile	Pro	Glu	His	Glu	Thr	Leu	Val	Leu	Lys						
				325					330										

<210> 9

<211> 435

<212> DNA

<213> Mus musculus

<220>

<221> misc\_feature

<222> (1)...(435)

<223> n = A,T,C or G

<400> 9

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tgtaatttg	cctattgttc	acacccttgt	ggccgctacc	aacagtttac	tttgtctggt	180
tacttctcga	ctggaagact	ccagataaag	gtggcaggcg	ttcagactgg	gtacggaact	240
ggaatgtctg	gaaccacatc	agggactatt	tccccattac	aatcctgaag	actaaggacc	300
tgtcaccttc	agagaactac	atcatggggg	tccaccccat	nggtctcctg	accttcggtg	360
ccttctgcaa	cttctgcact	gaggccacag	gcttctcgaa	gaccttccca	ggcatcactc	420
ctcacttggc	cacac					435

<210> 10

<211> 229

<212> PRT

<213> Mus musculus.

<400> 10

Met	Lys	Thr	Glu	His	Leu	Gln	Ser	Leu	Ser	Leu	Leu	Gln	Trp	Pro	Leu				
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Ser	Tyr	Val	Ala	Met	Phe	Trp	Ile	Val	Gln	Pro	Leu	Leu	Ile	Cys	Leu				
			20					25					30						
Leu	Phe	Thr	Pro	Leu	Trp	Pro	Leu	Pro	Thr	Val	Tyr	Phe	Val	Trp	Leu				
			35				40					45							
Leu	Leu	Asp	Trp	Lys	Thr	Pro	Asp	Lys	Gly	Gly	Arg	Arg	Ser	Asp	Trp				
			50			55					60								
Val	Arg	Asn	Trp	Asn	Val	Trp	Asn	His	Ile	Arg	Asp	Tyr	Phe	Pro	Ile				
65				70						75				80					
Thr	Ile	Leu	Lys	Thr	Lys	Asp	Leu	Ser	Pro	Ser	Glu	Asn	Tyr	Ile	Met				
			85					90						95					
Gly	Val	His	Pro	His	Gly	Leu	Leu	Thr	Phe	Gly	Ala	Phe	Cys	Asn	Phe				
			100					105					110						
Cys	Thr	Glu	Ala	Thr	Gly	Phe	Ser	Lys	Thr	Phe	Pro	Gly	Ile	Thr	Pro				
			115				120				125								
His	Leu	Ala	Thr	Leu	Ser	Trp	Phe	Phe	Lys	Ile	Pro	Ile	Ile	Arg	Asp				
			130			135					140								
Tyr	Ile	Met	Ala	Lys	Gly	Leu	Cys	Ser	Val	Ser	Gln	Ala	Ser	Ile	Asp				
145				150						155				160					
Tyr	Leu	Leu	Ser	His	Gly	Thr	Gly	Asn	Leu	Val	Gly	Ile	Pro	Ile	Ile				
				165				170					175						
Thr	Val	Val	Gly	Glu	Ala	Leu	Pro	Leu	Pro	Gln	Val	Lys	Asn	Pro	Ser				



115	120	125
Thr Phe Pro Gly Ile Thr Pro His Leu Ala Thr Leu Ser Trp Phe Phe		
130	135	140
Lys Ile Pro Phe Val Arg Glu Tyr Leu Met Ala Lys Gly Val Cys Ser		
145	150	155
Val Ser Gln Pro Ala Ile Asn Tyr Leu Leu Ser His Gly Thr Gly Asn		
165	170	175
Leu Val Gly Ile Val Val Gly Gly Val Gly Glu Ala Leu Gln Ser Val		
180	185	190
Pro Asn Thr Thr Thr Leu Ile Leu Gln Lys Arg Lys Gly Phe Val Arg		
195	200	205
Thr Ala Leu Gln His Gly Ala Tyr Leu Val Pro Ser Tyr Ser Phe Gly		
210	215	220
Glu Asn Glu Val Phe Asn Gln Glu Thr Phe Pro Glu Gly Thr Trp Leu		
225	230	235
Arg Leu Phe Gln Lys Thr Phe Gln Asp Thr Phe Lys Lys Ile Leu Gly		
245	250	255
Leu Asn Phe Cys Thr Phe His Gly Arg Gly Phe Thr Arg Gly Ser Trp		
260	265	270
Gly Phe Leu Pro Phe Asn Arg Pro Ile Thr Thr Val Val Gly Glu Pro		
275	280	285
Leu Pro Ile Pro Arg Ile Lys Arg Pro Asn Gln Lys Thr Val Asp Lys		
290	295	300
Tyr His Ala Leu Tyr Ile Ser Ala Leu Arg Lys Leu Phe Asp Gln His		
305	310	315
Lys Val Glu Tyr Gly Leu Pro Glu Thr Gln Glu Leu Thr Ile Thr		
325	330	335

<210> 13

<211> 1872

<212> DNA

<213> Homo sapiens

<400> 13

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gcgcggggaa	cggagtcctc	ctctgtcgcc	caggctggag	tgcaatggtg	caatctcagc	360
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tctgctgact	cataaaggca	caggcaacat	ggtcattgtg	gtgattggtg	gactggctga	1380

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cctctatgat cagcacatgt tcaactcctgg tggctttgtc aaccgcttcc agaagtgggt 1560
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tgccctacgt aaactgtttg accagcataa gaccaagttt ggtatctcag agaccagga 1800
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<210> 14
<211> 333
<212> PRT
<213> Homo sapiens

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Ile Ala Val Asn Leu Tyr Leu Val Val Phe Thr Pro Tyr Trp Pro Val
 35          40          45
Thr Val Leu Ile Leu Thr Trp Leu Ala Phe Asp Trp Lys Thr Pro Gln
 50          55          60
Arg Gly Gly Arg Arg Phe Thr Cys Val Arg His Trp Arg Leu Trp Lys
 65          70          75          80
His Tyr Ser Asp Tyr Phe Pro Leu Lys Leu Leu Lys Thr His Asp Ile
 85          90          95
Cys Pro Ser Arg Asn Tyr Ile Leu Val Cys His Pro His Gly Leu Phe
100          105          110
Ala His Gly Trp Phe Gly His Phe Ala Thr Glu Ala Ser Gly Phe Ser
115          120          125
Lys Ile Phe Pro Gly Ile Thr Pro Tyr Ile Leu Thr Leu Gly Ala Phe
130          135          140
Phe Trp Met Pro Phe Leu Arg Glu Tyr Val Met Ser Thr Gly Ala Cys
145          150          155          160
Ser Val Ser Arg Ser Ser Ile Asp Phe Leu Leu Thr His Lys Gly Thr
165          170          175
Gly Asn Met Val Ile Val Val Ile Gly Gly Leu Ala Glu Cys Arg Tyr
180          185          190
Ser Leu Pro Gly Ser Ser Thr Leu Val Leu Lys Asn Arg Ser Gly Phe
195          200          205
Val Arg Met Ala Leu Gln His Gly Val Pro Leu Ile Pro Ala Tyr Ala
210          215          220
Phe Gly Glu Thr Asp Leu Tyr Asp Gln His Ile Phe Thr Pro Gly Gly
225          230          235          240
Phe Val Asn Arg Phe Gln Lys Trp Phe Gln Ser Met Val His Ile Tyr
245          250          255
Pro Cys Ala Phe Tyr Gly Arg Gly Phe Thr Lys Asn Ser Trp Gly Leu
260          265          270
Leu Pro Tyr Ser Arg Pro Val Thr Thr Ile Val Gly Glu Pro Leu Pro
275          280          285
Met Pro Lys Ile Glu Asn Pro Ser Gln Glu Ile Val Ala Lys Tyr His
290          295          300
Thr Leu Tyr Ile Asp Ala Leu Arg Lys Leu Phe Asp Gln His Lys Thr
305          310          315          320
Lys Phe Gly Ile Ser Glu Thr Gln Glu Leu Glu Ile Ile

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<210> 15  
 <211> 1050  
 <212> DNA  
 <213> Homo sapiens

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 ttctccttct tggcactggg taagatctgc actgtgggct tcatagccct cctgtttaca 180  
 agattctggc tcctcactgt cctgtatgcg gcctgggtgg atctggaccg agacaagcca 240  
 cggcaggggg gccggcacat ccaggccatc aggtgctgga ctatatggaa gtacatgaag 300  
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 agcacaggct tctcttcgat ctccccgggt atccgcccc atctgatgat gctgaccttg 480  
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<210> 16  
 <211> 333  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
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 20 25 30  
 Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg Phe Trp Leu  
 35 40 45  
 Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg Asp Lys Pro  
 50 55 60  
 Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp Thr Ile Trp  
 65 70 75 80  
 Lys Tyr Met Lys Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr Ala Glu  
 85 90 95  
 Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro His Gly Val  
 100 105 110  
 Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser Thr Gly Phe  
 115 120 125  
 Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met Leu Thr Leu  
 130 135 140  
 Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser Ala Gly Leu  
 145 150 155 160  
 Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn Arg Lys Gly  
 165 170 175  
 Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln Glu Ala Leu  
 180 185 190

Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn Arg Lys Gly  
 195 200 205  
 Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val Pro Ile Phe  
 210 215 220  
 Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn Ser Ser Gly  
 225 230 235 240  
 Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile Met Gly Ile  
 245 250 255  
 Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr Ser Phe Gly  
 260 265 270  
 Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Gly Lys Pro Ile Glu  
 275 280 285  
 Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val Asn Gln Leu His  
 290 295 300  
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 305 310 315 320  
 Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe Cys  
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<210> 17  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic peptide

<400> 17  
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<210> 18  
 <211> 1233  
 <212> DNA  
 <213> Homo sapiens

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 gagatggggc actggatcca gcatcctctc cgccctccag gacctcttct ctgtcacctg 180  
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1233